

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/682,667

DATE: 10/09/2001

TIME: 06:44:24

Input Set : C:\Crf3\Datahold\EFS\09682667\Seqlist.txt

Output Set: N:\CRF3\10092001\I682667.raw

ENTERED

4 <110> APPLICANT: Hsueh, Aaron J.W.
5 Hsu, Sheau Yu
8 <120> TITLE OF INVENTION: MAMMALIAN PRO-APOPTOTIC BOK GENES AND
9 THEIR USES
11 <130> FILE REFERENCE: STAN072CON
13 <140> CURRENT APPLICATION NUMBER: 09/682,667
C--> 14 <141> CURRENT FILING DATE: 2001-10-05
16 <150> PRIOR APPLICATION NUMBER: 09/517,358
17 <151> PRIOR FILING DATE: 2000-03-02
19 <150> PRIOR APPLICATION NUMBER: 09/186,250
20 <151> PRIOR FILING DATE: 1998-11-04
22 <150> PRIOR APPLICATION NUMBER: 60/064,943
23 <151> PRIOR FILING DATE: 1997-11-07
25 <160> NUMBER OF SEQ ID NOS: 18
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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30 <211> LENGTH: 642
31 <212> TYPE: DNA
32 <213> ORGANISM: r. rattus
34 <400> SEQUENCE: 1
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36 tgcgccacag acaaggagct ggtggcccag gctaaagcac taggccgga gtacgtgcac 120
37 gcgcggttt tgcgcgcgg cctctcctgg agcgtccag agcgtgcctc gcctgcccct 180
38 ggaggacgcc tggcagaggt gtgcaccgtg ctgctgcgt tgggagatga gctggagcag 240
39 atccgtccca gcgtatatcg gaatgtggcc cggcagctgc acatccccct gcagtctgag 300
40 cctgtggtga ctgatgcctt cctcgtctgt gccggccaca tcttctcagc aggtatcaca 360
41 tggggcaagg tagtgtccct gtactcgggt gctgcgggac tagcgggtga ctgcgtccgg 420
42 caagctcagc cagccatggt tcatgccctg gttgactgcc tgggggaatt tgtacgcaag 480
43 accctggcca cctggcttcg gaggcgtggt ggatggacgg acgtcctcaa gtgtgtggtc 540
44 agcacagacc ctggcttcctg ctcccactgg ctcgtggcca cactctgcag ctttggccgc 600
45 ttcctgaagg ctgcattctt cctcctgttg ccagagagat ga 642
47 <210> SEQ ID NO: 2
48 <211> LENGTH: 213
49 <212> TYPE: PRT
50 <213> ORGANISM: r. rattus
52 <400> SEQUENCE: 2
53 Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp
54 1 5 10 15
55 Ala Phe Asp Arg Ser Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys
56 20 25 30
57 Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
58 35 40 45
59 Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
60 50 55 60
61 Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Gln
62 65 70 75 80
63 Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Pro

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| | | | | | | | |
|-----|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|
| 64 | | 85 | | 90 | | 95 | |
| 65 | Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly | | | | | | |
| 66 | | 100 | | 105 | | 110 | |
| 67 | His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr | | | | | | |
| 68 | | 115 | | 120 | | 125 | |
| 69 | Ser Val Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro | | | | | | |
| 70 | | 130 | | 135 | | 140 | |
| 71 | Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys | | | | | | |
| 72 | 145 | | 150 | | 155 | | 160 |
| 73 | Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu | | | | | | |
| 74 | | 165 | | 170 | | 175 | |
| 75 | Lys Cys Val Val Ser Thr Asp Pro Gly Phe Arg Ser His Trp Leu Val | | | | | | |
| 76 | | 180 | | 185 | | 190 | |
| 77 | Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Leu | | | | | | |
| 78 | | 195 | | 200 | | 205 | |
| 79 | Leu Leu Pro Glu Arg | | | | | | |
| 80 | 210 | | | | | | |
| 83 | <210> SEQ ID NO: 3 | | | | | | |
| 84 | <211> LENGTH: 513 | | | | | | |
| 85 | <212> TYPE: DNA | | | | | | |
| 86 | <213> ORGANISM: r.rattus | | | | | | |
| 88 | <220> FEATURE: | | | | | | |
| 89 | <221> NAME/KEY: CDS | | | | | | |
| 90 | <222> LOCATION: (1)...(513) | | | | | | |
| 92 | <400> SEQUENCE: 3 | | | | | | |
| 93 | atg gag gtg ctg cgg cgc tct tct gtc ttc gct gcg gag atc atg gac | | | | | | 48 |
| 94 | Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp | | | | | | |
| 95 | 1 | 5 | | 10 | | 15 | |
| 97 | gcc ttt gat cgc tcg ccc aca gac aag gag ctg gtg gcc cag gct aaa | | | | | | 96 |
| 98 | Ala Phe Asp Arg Ser Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys | | | | | | |
| 99 | | 20 | | 25 | | 30 | |
| 101 | gca cta ggc cgg gag tac gtg cac gcg cgg ctt ttg cgc gcc ggc ctc | | | | | | 144 |
| 102 | Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu | | | | | | |
| 103 | | 35 | | 40 | | 45 | |
| 105 | tcc tgg agc gct cca gag cgt gcc tcg cct gcc cct gga gga cgc ctg | | | | | | 192 |
| 106 | Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu | | | | | | |
| 107 | | 50 | | 55 | | 60 | |
| 109 | gca gag gtg tgc acc gtg ctg ctg cgc ttg gga atc aca tgg ggc aag | | | | | | 240 |
| 110 | Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys | | | | | | |
| 111 | 65 | 70 | | 75 | | 80 | |
| 113 | gta gtg tcc ctg tac tcg gtg gct gcg gga cta gcg gtg gac tgc gtc | | | | | | 288 |
| 114 | Val Val Ser Leu Tyr Ser Val Ala Ala Gly Leu Ala Val Asp Cys Val | | | | | | |
| 115 | | 85 | | 90 | | 95 | |
| 117 | cgg caa gct cag cca gcc atg gtt cat gcc ctg gtt gac tgc ctg ggg | | | | | | 336 |
| 118 | Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly | | | | | | |
| 119 | | 100 | | 105 | | 110 | |
| 121 | gaa ttt gta cgc aag acc ctg gcc acc tgg ctt cgg agg cgt ggt gga | | | | | | 384 |
| 122 | Glu Phe Val Arg Lys Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly | | | | | | |
| 123 | | 115 | | 120 | | 125 | |

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125 tgg acg gac gtc ctc aag tgt gtg gtc agc aca gac cct ggc ttc cgc      432
126 Trp Thr Asp Val Leu Lys Cys Val Val Ser Thr Asp Pro Gly Phe Arg
127      130                      135                      140
129 tcc cac tgg ctc gtg gcc aca ctc tgc agc ttt ggc cgc ttc ctg aag      480
130 Ser His Trp Leu Val Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys
131 145                      150                      155                      160
133 gct gca ttc ttc ctc ctg ttg cca gag aga tga      513
134 Ala Ala Phe Phe Leu Leu Leu Pro Glu Arg *
135                      165                      170
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 170
140 <212> TYPE: PRT
141 <213> ORGANISM: r.rattus
143 <400> SEQUENCE: 4
144 Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp
145 1                      5                      10                      15
146 Ala Phe Asp Arg Ser Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys
147      20                      25                      30
148 Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
149      35                      40                      45
150 Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
151      50                      55                      60
152 Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys
153 65                      70                      75                      80
154 Val Val Ser Leu Tyr Ser Val Ala Ala Gly Leu Ala Val Asp Cys Val
155      85                      90                      95
156 Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly
157      100                     105                     110
158 Glu Phe Val Arg Lys Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly
159      115                     120                     125
160 Trp Thr Asp Val Leu Lys Cys Val Val Ser Thr Asp Pro Gly Phe Arg
161      130                     135                     140
162 Ser His Trp Leu Val Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys
163 145                      150                      155                      160
164 Ala Ala Phe Phe Leu Leu Leu Pro Glu Arg
165                      165                      170
168 <210> SEQ ID NO: 5
169 <211> LENGTH: 642
170 <212> TYPE: DNA
171 <213> ORGANISM: H.sapiens
173 <220> FEATURE:
174 <221> NAME/KEY: CDS
175 <222> LOCATION: (1)...(642)
177 <400> SEQUENCE: 5
178 atg gag gtg ctg cgg cgc tct tcg gtc ttc gct gcg gag atc atg gac      48
179 Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp
180 1                      5                      10                      15
182 gcc ttt gat cgc tgg ccc aca gac aag gag ctg gtg gcc cag gct aaa      96
183 Ala Phe Asp Arg Trp Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys

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184          20          25          30
186 gca cta ggc cgg gag tac gtg cac gcg cgg ctt ttg cgc gcc ggc ctc      144
187 Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
188          35          40          45
190 tcc tgg agc gct cca gag cgt gcc tcg cct gcc cct gga gga cgc ctg      192
191 Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
192          50          55          60
194 gca gag gtg tgc acc gtg ctg ctg cgc ttg gga gat gag ctg gag cag      240
195 Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Gln
196          65          70          75          80
198 atc cgt ccc agc gta tat cgg aat gtg gcc cgg cag ctg cac atc cct      288
199 Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Pro
200          85          90          95
202 ctg cag tct gag cct gtg gtg act gat gcc ttc ctc gct gtg gcc ggc      336
203 Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly
204          100          105          110
206 cac atc ttc tca gca ggt atc aca tgg ggc aag gta gtg tcc ctg tac      384
207 His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr
208          115          120          125
210 tcg gcg gct gcg gga cta gcg gtg gac tgc gtc cgg caa gct cag cca      432
211 Ser Ala Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro
212          130          135          140
214 gcc atg gtt cat gcc ctg gtt gac tgc ctg ggg gaa ttt gta cgc aag      480
215 Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys
216          145          150          155          160
218 acc ttg gct acc tgg ctt cgg agg cgt ggt gga tgg acg gac gtc ctc      528
219 Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu
220          165          170          175
222 aag tgt gtg gtc agc aca aaa cct ggc ttc cgc tcc cac tgg ctc gtg      576
223 Lys Cys Val Val Ser Thr Lys Pro Gly Phe Arg Ser His Trp Leu Val
224          180          185          190
226 gcc aca ctc tgc agc ttt ggc cgc ttc ctg aag gct gca ttc ttc ctc      624
227 Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Leu
228          195          200          205
230 ctg ttg cca gag aga tga      642
231 Leu Leu Pro Glu Arg *
232          210
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 213
237 <212> TYPE: PRT
238 <213> ORGANISM: H.sapiens
240 <400> SEQUENCE: 6
241 Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp
242          1          5          10          15
243 Ala Phe Asp Arg Trp Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys
244          20          25          30
245 Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
246          35          40          45
247 Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu

```

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248      50      55      60
249 Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Asp Glu Leu Glu Gln
250 65      70      75      80
251 Ile Arg Pro Ser Val Tyr Arg Asn Val Ala Arg Gln Leu His Ile Pro
252      85      90      95
253 Leu Gln Ser Glu Pro Val Val Thr Asp Ala Phe Leu Ala Val Ala Gly
254      100      105      110
255 His Ile Phe Ser Ala Gly Ile Thr Trp Gly Lys Val Val Ser Leu Tyr
256      115      120      125
257 Ser Ala Ala Ala Gly Leu Ala Val Asp Cys Val Arg Gln Ala Gln Pro
258      130      135      140
259 Ala Met Val His Ala Leu Val Asp Cys Leu Gly Glu Phe Val Arg Lys
260 145      150      155      160
261 Thr Leu Ala Thr Trp Leu Arg Arg Arg Gly Gly Trp Thr Asp Val Leu
262      165      170      175
263 Lys Cys Val Val Ser Thr Lys Pro Gly Phe Arg Ser His Trp Leu Val
264      180      185      190
265 Ala Thr Leu Cys Ser Phe Gly Arg Phe Leu Lys Ala Ala Phe Phe Leu
266      195      200      205
267 Leu Leu Pro Glu Arg
268      210
271 <210> SEQ ID NO: 7
272 <211> LENGTH: 513
273 <212> TYPE: DNA
274 <213> ORGANISM: H. sapiens
276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (1)...(513)
280 <400> SEQUENCE: 7
281 atg gag gtg ctg cgg cgc tct tcg gtc ttc gct gcg gag atc atg gac      48
282 Met Glu Val Leu Arg Arg Ser Ser Val Phe Ala Ala Glu Ile Met Asp
283 1      5      10      15
285 gcc ttt gat cgc tgg ccc aca gac aag gag ctg gtg gcc cag gct aaa      96
286 Ala Phe Asp Arg Trp Pro Thr Asp Lys Glu Leu Val Ala Gln Ala Lys
287      20      25      30
289 gca cta ggc cgg gag tac gtg cac gcg cgg ctt ttg cgc gcc ggc ctc      144
290 Ala Leu Gly Arg Glu Tyr Val His Ala Arg Leu Leu Arg Ala Gly Leu
291      35      40      45
293 tcc tgg agc gct cca gag cgt gcc tcg cct gcc cct gga gga cgc ctg      192
294 Ser Trp Ser Ala Pro Glu Arg Ala Ser Pro Ala Pro Gly Gly Arg Leu
295      50      55      60
297 gca gag gtg tgc acc gtg ctg ctg cgc ttg gga atc aca tgg ggc aag      240
298 Ala Glu Val Cys Thr Val Leu Leu Arg Leu Gly Ile Thr Trp Gly Lys
299 65      70      75      80
301 gta gtg tcc ctg tac tcg gcg gct gcg gga cta gcg gtg gac tgc gtc      288
302 Val Val Ser Leu Tyr Ser Ala Ala Ala Gly Leu Ala Val Asp Cys Val
303      85      90      95
305 cgg caa gct cag cca gcc atg gtt cat gcc ctg gtt gac tgc ctg ggg      336
306 Arg Gln Ala Gln Pro Ala Met Val His Ala Leu Val Asp Cys Leu Gly

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VERIFICATION SUMMARY

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Input Set : C:\Crf3\Datahold\EFS\09682667\Seqlist.txt

Output Set: N:\CRF3\10092001\I682667.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date